Bio-Conf Septembre 2015

Je 27/8 11h CBP-LR6-23 — **Jose Paulo FARINHA** — **"Very bright, very stable: very useful"**

External seminar

Laboratoire Joliot-Curie

(Centro de Quimica-Fisica Molecular & Institute of Nanosciences and Nanotechnology, IST, University of Lisbon, Portugal)
Contact : Marie-Thérèse CHARREYRE, marie-therese.charreyre@ens-lyon.fr

Luminescent nanomaterials are used in many applications, from advanced imaging techniques to biodiagnostic, etc. The ability to increase the brightness and photostability of these materials have direct impact on their performance, lowering the limit of detection in diagnostic applications and allowing their use in demanding laser scanning imaging techniques. This communication will focus on the use of different approaches to obtain highly fluorescent materials, based on polymers, silica nanoparticles and hybrid nanostructures.

Je 3/9 11h00 IBCP conf. — **Stephan UPHOFF** — **"Stochastic activation of a DNA damage response causes cell-to-cell mutation rate variation"**

External seminar

IBCP — BMSI UMR 5086

(Dept. of Biochemistry, University of Oxford, UK)

To protect their genome, cells rely on the precise action of proteins that detect and repair DNA damage. However, noise in gene expression fundamentally limits the fidelity of cell processes, and transient fluctuations in the concentrations of DNA repair enzymes could result in permanent genetic changes. Here we investigated variation of the Ada protein that auto-induces the adaptive response to DNA alkylation damage in Escherichia coli. We found that undamaged cells on average produce a single Ada molecule per generation. Sudden damage conditions therefore find many cells trapped in a state with zero Ada molecules, which inevitably delays the damage response until the first random expression event occurs. This can take several generations and creates a distinct subpopulation of cells with elevated mutation rates. Non-genetic variation in protein levels can thus lead to genetic heterogeneity in the population. However, because the adaptive response is remarkably precise given the low abundances involved, and high Ada expression is toxic to cells, we hypothesize that the stochastic activation is not a manifestation of an evolutionary bet-hedging strategy but is driven by a short-term trade-off between the need to reliably repair damage while minimizing harmful side effects.

Lu 7/9 11h00 SdT CRC — **Yehu MORAN** — **"Elucidating the evolution of post-transcriptional regulation via the cnidarian microRNA pathway"**

Seminaire Externe

igfl

(Univ. Jerusalem)
Hôte : A GILLES - IGFL

Ma 15/9 the day Domaine Rockfeller — **Viroscand3D-Profilexpert** — **"Le NGS en infectiologie "**

workshop

ViroScan3D Genomic Solutions for Infectious Diseases

ProfileXpert

contact: C. Lachuer

Le séquençage nouvelle génération (NGS). Le séquençage nouvelle génération (NGS) a révolutionné le domaine de l'infectiologie tant en recherche fondamentale, clinique qu'industrielle. Dans le domaine de la recherche, on peut citer le séquençage de génomes procaryotes, viraux, bactériens, de microbiomes, viromes, de génomes eucaryotes (réservoirs, vecteurs ou hôtes), la recherche d'agents infectieux inconnus, l'identification et le suivi d'agents infectieux en épidémiologie, le génotypage de mutants de résistance (Pathogen Discovery).
En ce qui concerne la partie clinique ou diagnostique, la recherche de biomarqueurs moléculaires diagnostiques, pronostiques, thérapeutiques, la compréhension des mécanismes géniques, ou épigénomiques (Biomarker Discovery) utilisent le NGS comme méthode de routine. Il est probable que le NGS puisse également dans un futur proche, être la méthode de référence pour la recherche d'agents contaminants dans des préparations à destinée humaine ou animale (Biosafety).
Dans ce contexte, nous aborderons lors de ce colloque, différents thèmes portant sur ces aspects de Biomarker Discovery, Pathogen Discovery et Biosafety spécifiquement appliqués au domaine de l'infectiologie.
L'agenda préliminaire est visible sur notre site: http://eventregistration.illumina.com/events/le-ngs-en-infectiologie-lyon-15-septembre-2015/event-summary-16424be6266e41848e211d53a71f3603.aspx

Je 24/9 11h00 SdT CRC — **Pr. Jean-Michel CLAVERIE** — **"Giant Viruses !"**

FORUM INFECTIOLOGIE

(Head, Mediterranean Institute of Microbiology (IMM, FR3479 CNRS-AMU); Director, Structural & Genomic Information Lab. (IGS, UMR7256 CNRS-AMU))
Contact: Henri GRUFFAT (henri.gruffat@inserm.fr)

More than a century ago, the notion of "virus" was introduced to designate infectious agents invisible to the light microscope and capable of passing through "sterilizing" filters. In addition to their extremely small size, most viruses studied over the years also exhibited minimal genomes and gene contents, almost entirely relying on cell-encoded functions to multiply, as expected from absolute intracellular parasites. Unexpectedly, the last ten years have seen the discovery of 4 different families of eukaryotic "giant viruses" exhibiting particles of cellular dimensions as well as gene contents overlapping in size with that of bacteria and some parasitic eukaryotes. Although all presently known giant viruses have been isolated using Acanthamoeba as laboratory host, related members are now starting to be found in other protozoa, such as marine picoplankton species the population of which they regulate. Representatives of two families of giant viruses have been revived from a layer of Siberian permafrost radiocarbon dated from 30.000 years ago, raising concern that pathogenic viruses from long past epidemics might also remain infectious and resurface in circumpolar regions as a consequence of global warming and industrial exploitations.

The unexpected abundance, ubiquity and diversity of giant viruses, as well as the alien nature of their gene contents deeply challenge conventional conceptions about the origin and evolution of all DNA viruses and raise the question of their evolutionary relationship with the 3 cellular domains forming today's Tree of Life, and possibly other long extinct cellular lineages.

Ve 25/9 11h00 AP-CERVI — **Prof Yuji C. SASAKI** — **"3D Dynamical Observations of Single Molecule Internal motions by X-rays, Electron, and Neutron"**

Séminaire Externe

(Graduate School of Frontier Sciences, The University of Tokyo - JAPON)
Contact: Jean-François NICOLAS – jean-francois.nicolas@inserm.fr

We have proposed single molecule techniques using short wavelength probes, such as X-rays, electrons, and neutron. In this presentation, I will introduce single molecular dynamics observation techniques that are developed in our lab and discuss possible applications. Especially, Diffracted X-Ray Tracking (DXT) using normal synchrotron orbital radiation source has been developed for obtaining the information of the 3D internal motions of single protein molecules with both high time-resolution (micro-seconds) and high precision (nm/1000). DXT is a method to obtain three-dimensional (3D) dynamics through trajectories of the Laue diffraction spots from the labelled individual gold nanocrystal. This concept can be applied to utilize also with electrons or neutrons. DXT can be used to trace functional internal motions of protein at single molecule level in two rotational axes, tilting and twisting views. Until now, we are trying to observe Brownian motions of individual DNA molecules, actin-myosin interactions, denatured proteins, functional protein membranes (bacteriorhodopsin, AChBP, AChR, and KvAP), antigen-antibody interactions, peptide/MHC complex for T cell activation, and monitoring super-weak force (pN) using Super-high-speed DXT. Next, we try to observe the structural fluctuations of intrinsically disordered proteins (IDP), for example, tau proteins in Alzheimer paired helical filaments-like fibers, alpha-synuclein which is of great interest to Parkinson's researchers. Additionally, we have applied DXT method as a high time resolution (1-10μs) and high positional accuracy (-pm) detection system for the time-resolved dynamical interactions between a single gold nanocrystal and localized individual super-saturated molecule networks

Me 30/9 11h SdT CRC — **François-Xavier LAURENT** — **La génétique au service de la criminalistique et inversement**

Seminaire Externe

(Responsable Recherche & Développement - Institut National de Police Scientifique (INPS))

Contact : isabelle.grosjean@ibcp.fr

L'Institut National de Police Scientifique (INPS) est l'un des acteurs majeurs concernant l'identification criminelle : prélèvements sur individus et exploitations de traces biologiques. Notre expertise s'étend désormais à l'authentification de lignées cellulaires humaines. Cette certification est de plus en plus demandée pour la publication de travaux dans les journaux scientifiques.
La première partie du séminaire présentera ce service : établissement de profils génétiques STR, comparaison aux bases de données internationales et calcul de match. La seconde partie du séminaire abordera les projets
R&D de l'Institut visant au développement de méthodes d'analyses génétiques innovantes dans le cadre d'enquêtes criminelles en cours : identification de fluides biologiques, différenciation de jumeaux homozygotes, portrait-robot génétique.

Code lieu	
SdT CRC	*Salle des Thèses Chantal Rabourdin-Combe*
ss LR5	*Salle de Réunion du Sous-sol LR5*
CBP-LR6-23	*salle CO23 du CBP rez-de-chaussée LR6*
AP-CERVI	* *Amphi Pasteur CERVI* *
IGFL 063 rdc	*Salle 063 au RDC de l'IGFL*
IBCP Conf.	*IBCP Confernce Room level -1*

* carte d'identité obligatoire pour entrer sur le site

A Venir

Me-Ve 18-20/11/2015 9h00 — **Lyon SysBio 2015** — http://lyonsysbio2015.sciencesconf.org/?lang=en

International conference

Contact: François Briat
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LyonSysBio is the yearly international conference organized by BioSyL (http://lyonsysbio2015.sciencesconf.org/?lang=en), the Systems Biology Alliance of Lyon.
Its goal is to promote exchanges between scientists from different fields (biology, mathematics, computer sciences, physics, social sciences…) interested in the analysis of the wealth of data generated by modern biology, as well as the construction of the necessary modeling tools to gain system level thoughtful insights.
In 2015, the conference will be held from the 18th to the 20th of November in Lyon. It will be dedicated to discussions around the 4 following themes: systems immunology, cell differentiation, a systems view on genotype-phenotype relationship and microbiological systems biology. Keynote lectures will be delivered by the following speakers:
Gregoire Altan-Bonnet (MSK cancer center, New-York)
Becca Asquith (Imperial College, London)
Chris Bakal (Institute of cancer research, London)
Sckjoon Jun (University of California, San Diego)
James Locke (University of Cambridge)
John Marioni (European Bioinformatics Institute, Cambridge)
Carsten Peterson (Computational Biology & Biological Physics, Lund University, Sweden)
Andreas Wagner (IEU, University of Zurich)